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(h) sequencing an isolated member nucleic acid molecule, thereby identifying a nucleic acid sequence.

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30. (Amended) The method of claim 29, wherein the cDNA molecules comprise a second library selected from the group consisting of a collection of sequences derived from the 5' end of RNA molecules, a collection of sequences derived from the internal regions of RNA molecules, and a collection of sequences derived from the 3' end of RNA molecules.

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32. (Amended) The method of claim 27, wherein the population of nucleic acid molecules comprises genomic DNA.

33. (Amended) The method of claim 27, wherein the population of nucleic acid molecules comprises a normalized population of nucleic acids.

34. (Amended) The method of claim 27, wherein the set of nucleic acid molecules is fractionated from other nucleic acid molecules in the population of nucleic acid molecules by size.

35. (Amended) The method of claim 34, wherein said fractionation is by electrophoresis.

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38. (Amended) The method of claim 27, wherein members of the set of nucleic acid molecules differ from one another by 20 or fewer nucleotides in length.

39. (Amended) The method of claim 27, wherein members of the set of nucleic acid molecules differ from one another by 15 or fewer nucleotides in length.

40. (Amended) The method of claim 27, wherein members of the set of nucleic acid molecules differ from one another by 12 or fewer nucleotides in length.

41. (Amended) The method of claim 27, wherein members of the set of nucleic acid molecules differ from one another by 8 or fewer nucleotides in length.

42. (Amended) The method of claim 27, wherein members of the set of nucleic acid molecules by 6 differ from one another or fewer nucleotides in length.

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43. (Amended) The method of claim 27, wherein the population of nucleic acid molecules comprises nucleic acids having terminal sequences identical to those produced by digestion of a nucleic acid molecule with one or more restriction endonucleases.

44. (Amended) The method of claim 43, wherein the restriction endonuclease is a Type II or Type IIS restriction endonuclease.

47. (Amended) The method of claim 27, wherein the first library is prepared by a process comprising:

- a5
- (a) ligating the isolated set of nucleic acid molecules to a vector to form a population of vector-insert nucleic acid molecules;
 - (b) transforming the vector-insert nucleic acid molecules into a host cell to form the first library; and
 - (c) culturing the first library under conditions that allow for at least some members of the first library to be distinguished from other members of the first library.

50. (Amended) The method of claim 27, wherein two or more member nucleic acid molecules are pooled prior to fractionating the recovered subset of nucleic acid molecules.

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51. (Amended) The method of claim 27, wherein the recovered subset of nucleic acid molecules is fractionated by size.

52. (Amended) The method of claim 27, wherein the recovered subset of nucleic acid molecules is fractionated by electrophoresis.

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54. (Amended) The method of claim 27, wherein the isolated member nucleic acid molecule is compared to one or more known nucleic acid sequences prior to sequencing.

Add the following new claims:

--56. A method of identifying a nucleic acid sequence, the method comprising:

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- (a) providing a population of nucleic acid molecules comprising at least one set of nucleic acid molecules;
 - (b) conducting a physical fractionation on the nucleic acid molecules in the population to provide the set of nucleic acid molecules;
 - (c) isolating the fractionated set of nucleic acid molecules;
 - (d) constructing a library with the isolated set of nucleic acid molecules, wherein the library comprises a subset of one or more member nucleic acid molecules;
 - (e) recovering nucleic acids comprising the subset from the library;
 - (f) fractionating the recovered subset from at least some of the other recovered nucleic acids, wherein the fractionation is carried out according to the size of the nucleic acids;
 - (g) isolating at least one member nucleic acid molecule from the subset of nucleic acid molecules fractionated by size; and
 - (h) sequencing an isolated member nucleic acid molecule, thereby identifying a nucleic acid sequence.

57. The method of claim 56 wherein the fractionating conducted in step (f) further comprises:

- (i) providing a plurality of mixtures, wherein each mixture is prepared by multiplexing a plurality of recovered nucleic acids;
- (ii) fractionating each mixture according to the size of the nucleic acids; and
- (iii) deconvoluting the sized nucleic acids occurring among the plurality of mixtures to provide at least one sized subset of nucleic acid molecules.--